

Amendments to the claims:

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified AvIII peptide with cellulase activity and, ~~said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme having at least 70 90% identity to SEQ ID NO. 1, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.~~, ~~the catalytic domain GH74_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII_Ace):~~

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GH74_Ace      AFTQPTWQVVAIGGGG FVDSIVFNGCAPGILVVRDGGCMRMBAAACRNIFLLDMWG
AvIII_Ace     AAGQAVTWQVVTGCGCGFTPGIVNPAKGVAVARTDGGAVRLNSDD TWTPLHENVG
* * * * *

GH74_Ace      WNNWGINGVVCIADDPINTNKWVAAVGMYTNSWDPNDCAILRSDQCATWQITPLPFKLG
AvIII_Ace     NPTWHDNGIDALATDPVDTDRVAVAVGMYTNSWDPNVGGILRSTDGGPTWFTTKLPFKVG
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GH74_Ace      CNMPCRCMGSR LAVDPNEDNELYFCAPGCKGLWRSTDCGATWCGMTNTFDVCTVIANDTD
AvIII_Ace     CNMPCRCMGSR LAVDPNNGTILYFCARGCHGLWRSTDYCATWSNVTSFTWTCTYFQDSGG
* * * * *

GH74_Ace      TPGVSSDIQCWVAWAFDKSSSLQNSKTIIFGVADPNPNVFWCRDGGATWQAVPGAP T
AvIII_Ace     T YTSDFVGIAMVTFBETSGCGGCGATTRIFGVADAGKGVTKGEBAGATWVAUSCEPQV
* * * * *

GH74_Ace      GPFPKGVTFDPVNHVLYIATGNTGCPYDCSSCDVHKFSUTSCTWTRISDPDSTDIANDYP
AvIII_Ace     GFLPHKCVLSPEKTLVIGYANGAGPYDGTNGTAKVNTSGVMTDISP TGLASTFY
* * * * *

GH74_Ace      GYGLTIDRQHPTTIVATQICSWPDTIIFRSTDCGATNRIWDWISVNRSLAYVLDIS
AvIII_Ace     GYGLQVDLQVDCITLMVAALNCNWDDELIFRSTDCGATNCPINWNGYPCINVYVSYDIG
* * * * *

GH74_Ace      AEFWLTPGVQPNDFVPGPKLCMDDEAMAIDPFNSDRMLYCTGATLYATNBLTKWDSGGQI
AvIII_Ace     NADNIQDTTSTDGFE VRVGNMVEALAIIDPFDSNHWLYCTGLTVGGHDLTNWDSKHPV
* * * * *

GH74_Ace      HIRPWKGLSETAVNDLICTPPGAGPLIGALCDLCCETHADVTAVDPSTIFTSPVETTCISV
AvIII_Ace     TVKGLAVGIEEMAVLGLITPPGCRALLSAVCDGCFYHSDLDAAAPNQAVHTPTVCTNGI
* * * * *

GH74_Ace      DYAEINPGLIIVRAGSFDPSGQNDNVAFSTDCGHWPFQGGEPGGVTTCGTVAASAGGR
AvIII_Ace     DYACNKPENIVRSGAGDDYP TLAACGNPGCTWFDYAACTGTCTCAVALSADGDT
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GH74_Aac ----- FVWAPEDPCQPIVAVGFCNCHWALSCGVFANQGISDRVNDKTFYALCNGTFYRSTDDGV
AviIII_Aac ----- VLLMSSTGCAVSKSCG TLTAVSSLDGCAVIASDKSDNTFVYGGGACAIYVSIQTAT
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GH74_Aac ----- TFQPVIAGLPSSCAVGVMTHTAVPCKECDLWLAACSELVISTVGGGSGWAI TCVSSAVNV
AviIII_Aac ----- SFTKTFV LGGSTTVNAIR AHPGACDWAQCTDKLWISTDYCSTFTQICSGVTAGWCF
-----
GH74_Aac ----- CFCKSADGSCYPAVFVGTIGGVTCAYRSDDECTFWLINDDQHGVN WQATTCDHAN
AviIII_Aac ----- CFCKASCTGCVVTVYCEPTIDCAAGLFRKSDAGTNWQVIGDASNGFCSSGSAFVNGDLQT
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GH74_Aac ----- LRRVVECTNRCGIVVGBICGAPCG
AviIII_Aac ----- YCRVFRCHERTCHLLHSGQRBPAG
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2. (Previously Presented) The composition of claim 1 wherein the AviIII peptide is further defined as comprising a linker and a signal sequence.
3. (Cancelled)
4. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Previously Presented) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the AviIII peptide is further defined as comprising a length of about 90 amino acids.
6. (Previously Presented) The composition of claim 1 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide sequence identical to SEQ ID NO: 3.
7. (Previously Presented) The composition of claim 1 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.
8. (Previously Presented) The composition of claim 1 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.
9. (Previously Presented) The composition of claim 1 wherein said AviIII protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74_Ace has at least 90% sequence identity with SEQ ID NO: 3.

11. (Previously Presented) The composition of claim 1, wherein the catalytic domain of GH74 has at least 80% sequence identity with SEQ ID NO: 3.

12. (Previously Presented) An isolated AvIII peptide having a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Previously Presented) An industrial mixture suitable for degrading cellulose, such mixture comprising the AvIII polypeptide of claim 1.

15. (Currently Amended) The industrial mixture of claim 14 further defined as comprising a detergent.[.]

16-27 (Cancelled)

28. (Previously Presented) An isolated polypeptide molecule comprising at least one polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;
- c) a polypeptide sequence of SEQ ID NO: 5;
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

51. (New) The composition of claim 50 wherein said AvIII peptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (New) A composition comprising a substantially purified AvIII peptide having an amino acid sequence identical to SEQ ID NO. 1, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (New) A composition comprising a substantially purified AvIII peptide, said AvIII peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain GH74_Ace having a sequence that is at least 90% identical to SEQ ID NO. 3.

54. (New) The composition of claim 51 wherein said catalytic domain GH74_Ace has a sequence identical to SEQ ID NO. 3.